

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

ROBERTSON, Daniel E.
MURPHY, Dennis
REID, John
MAFFIA, Anthony
LINK, Steven
SWANSON, Ronald V.
WARREN, Patrick V.
KOSMOTKA, Anna

(ii) TITLE OF INVENTION:

ESTERASES

(iii) NUMBER OF SEQUENCES: 42

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN
(B) STREET: 6 BECKER FARM ROAD
(C) CITY: ROSELAND
(D) STATE: NEW JERSEY
(E) COUNTRY: USA
(F) ZIP: 07068

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 INCH DISKETTE
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: MS-DOS
(D) SOFTWARE: WORD PERFECT 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Unassigned
(B) FILING DATE: Concurrently
(C) CLASSIFICATION: Unassigned

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: HERRON, CHARLES J.
(B) REGISTRATION NUMBER: 28,019
(C) REFERENCE/DOCKET NUMBER: 331400-39

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-994-1700
(B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 52 NUCLEOTIDES
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGAGAATTC ATAAAGAGG AGAAATTAAAC TATGTCTTTA AACAAAGCACT CT

52

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 31 NUCLEOTIDES
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGGAAGATCT CTATCGTTA GTGTATGATT T

31

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 52 NUCLEOTIDES
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGAGAATTC ATAAAGAGG AGAAATTAAAC TATGAAACTC CTTGAGCCCCA CA

52

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 31 NUCLEOTIDES
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGAAGATCT CGCCGGTACA CCATCAGCCA C

31

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 52 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGAGAATTC ATAAAGAGG AGAAATTAAC TATGCCATAT GTTAGGAATG GT 52

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 53 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGAGGTACC TTAGAACTGT GCTGAAGAAA TAAATTCGTC CATTGCTCTA TTA 53

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 49 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGGAGGTACC TTAGAACTGT GCTGAAGAAA TAAATTCGTC CATTGCTCT 49

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 53 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGAGAATTC ATAAAGAGG AGAAATTAAC TATGAGATTG AGGAAATTG AAG 53

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGAGGTACC CTATTCAGAA AGTACCTCTA A

31

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 52 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCGAGAATTCTTAAAGAGGAGAAATTAACTATGTTTAATATCAATGTCTTT

52

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGGAAGATCT TTAAGGATTT TCCCTGGGTA G

31

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 52 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCGAGAATTCTTAAAGAGGAGAAATTAACTATGGAGGTTTACAAGGCCAAC

52

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGGAGGTACC TTATTGAGCC GAAGAGTACG A

31

(2) INFORMATION FOR SEQ ID NO:14:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 53 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCGAGAATTTC ATTAAAGAGG AGAAATTAAC TATGATTGGC AATTTGAAAT TGA

53

(2) INFORMATION FOR SEQ ID NO:15:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGGAGGTACC TTAAAGTGCT CTCATATCCC C

31

(2) INFORMATION FOR SEQ ID NO:16:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 31 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCGAGAATTTC ATTAAAGAGG AGAAATTAAC TATGCCAGCT AATGACTCAC CC

52

(2) INFORMATION FOR SEQ ID NO:17:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 32 NUCLEOTIDES
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGGAAGATCT TCAACAGGCT CCAAATAATT TC

32

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 29 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGGAAGATCT ACAGGCTCCA AATAATTTC

29

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 52 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCGAGAATTTC ATTAAAGAGG AGAAATTAAAC TATGCTTGAT ATGCCAATCG AC

52

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGGAGGTACC CTAGTCGAAC AGAAGAAGAG C

31

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 52 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGAGAATTTC ATTAAAGAGG AGAAATTAAAC TATGCCCTTA GATCCTAGAA TT

52

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 31 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGGAGGTACC TTAAATTTA TCATAAAAATA C

31

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 555 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: GENOMIC DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG TCT TTA AAC AAG CAC TCT TGG ATG GAT ATG ATA ATA TTT ATT CTC
Met Ser Leu Asn Lys His Ser Trp Met Asp Met Ile Ile Phe Ile Leu
1 5 10 15

48

AGC TTT TCT TTC CCA TTA ACA ATG ATC GCA TTA GCT ATC TCT ATG TCG
Ser Phe Ser Phe Pro Leu Thr Met Ile Ala Leu Ala Ile Ser Met Ser
20 25 30

96

TCA TGG TTT AAT ATA TGG AAT AAT GCA TTA AGC GAT CTA GGA CAT GCT
Ser Trp Phe Asn Ile Trp Asn Asn Ala Leu Ser Asp Leu Gly His Ala
35 40 45

144

GTT AAA AGC AGT GTT GCT CCA ATA TTC AAT CTA GGT CTT GCA ATT GGT
Val Lys Ser Ser Val Ala Pro Ile Phe Asn Leu Gly Leu Ala Ile Gly
50 55 60

192

GGG ATA CTA ATT GTT ATA GGT TTA AGA AAT CTT TAT TCG TGG AGT
Gly Ile Leu Ile Val Ile Gly Leu Arg Asn Leu Tyr Ser Trp Ser
65 70 75 80

240

AGA GTT AAA GGA TCT TTA ATC ATA TCC ATG GGT GTA TTT CTT AAC TTA
Arg Val Lys Gly Ser Leu Ile Ile Ser Met Gly Val Phe Leu Asn Leu
85 90 95

288

ATA GGG GTT TTC GAC GAA GTA TAT GGT TGG ATA CAT TTC CTA GTC TCA
Ile Gly Val Phe Asp Glu Val Tyr Gly Trp Ile His Phe Leu Val Ser
100 105 110

336

GTA TTG TTT TTC TTA TCA ATA ATA GCA TAT TTC ATA GCT ATA TCA ATA
Val Leu Phe Phe Leu Ser Ile Ile Ala Tyr Phe Ile Ala Ile Ser Ile
115 120 125

384

CTT GAC AAA TCA TGG ATA GCT GTT CTA CTA ATA ATA GGT CAT ATT GCA
Leu Asp Lys Ser Trp Ile Ala Val Leu Leu Ile Ile Gly His Ile Ala
130 135 140

432

ATG TGG TAT CTA CAC TTT GCT TCA GAG ATT CCG AGA GGT GCT GCT ATT

480

Met Trp Tyr Leu His Phe Ala Ser Glu Ile Pro Arg Gly Ala Ala Ile			
145	150	155	160
CCC GAG TTA TTA GCG GTA TTC TCG TTT TTA CCA TTC TAT ATA AGA CAG			528
Pro Glu Leu Leu Ala Val Phe Ser Phe Leu Pro Phe Tyr Ile Arg Asp			
165	170	175	
TAT TTT AAA TCA TAC ACT AAA CGA TAG			576
Tyr Phe Lys Ser Tyr Thr Lys Arg			
180			

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 1041 NUCLEOTIDES
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG AAA CTC CTT GAG CCC ACA AAT ACC TCC TAC ACG CTG TTA CAG GAT			48
Met Lys Leu Leu Glu Pro Thr Asn Thr Ser Tyr Thr Leu Leu Gln Asp			
1	5	10	15
TTA GCA TTG CAT TTT GCA TTT TAC TGG TTT CTG GCC GTG TAT ACG TGG			96
Leu Ala Leu His Phe Ala Phe Tyr Trp Phe Leu Ala Val TYr Thr Trp			
20	25	30	
TTA CCC GGT GTC CTA GTC CGG GGC GTA GCT GTG GAC ACA GGG GTG GCT			144
Leu Pro Gly Val Leu Val Arg Gly Val Ala Val Asp Thr Gly Val Ala			
35	40	45	
CGG GTG CCT GGG CTC GGC CGG CGC GGT AAG AGG CTG CTC CTG GCC GCT			192
Arg Val Pro Gly Leu Gly Arg Arg Gly Lys Arg Leu Leu Leu Ala Ala			
50	55	60	
GTG GCT GTC TTG GCG CTT GTT GTG TCC GTT GTC CCG GCT TAT GTG			240
Val Ala Val Leu Ala Leu Val Val Ser Val Val Val Pro Ala Tyr Val			
65	70	75	80
GCG TAT AGT AGT CTG CAC CCG GAG AGC TGT CGG CCC GTT GCG CCG GAG			288
Ala Tyr Ser Ser Leu His Pro Glu Ser Cys Arg Pro Val Ala Pro Glu			
85	90	95	
GGG CTC ACC TAC AAA GAG TTC AGC GTG ACC GCG GAG GAT GGC TTG GTG			336
Gly Leu Thr Tyr Lys Glu Phe Ser Val Thr Ala Glu Asp Gly Leu Val			
100	105	110	
GTT CGG GGC TGG GTG CTG GGC CCC GGC GCT GGG GGC AAC CCG GTG TTC			384
Val Arg Gly Trp Cal Leu Gly Pro Gly Ala Gly Gly Asn Pro Val Phe			
115	120	125	
GTT TTG ATG CAC GGG TAT ACT GGG TGC CGC TCG GCG CCC TAC ATG GCT			432
Val Leu Met His Gly Tyr Thr Gly Cys Arg Ser Ala Pro Tyr Met Ala			
130	135	140	
G TG CTG GCC CGG GAG CTC GTG GAG TGG GGG TAC CCG GTG GTT GTG TTC			480
Val Leu Ala Arg Glu Leu Val Glu Trp Gly Tyr Pro Val Val Val Phe			
145	150	155	160

GAC	TTC	CGG	GGC	CAC	GGG	GAG	AGC	GGG	GGC	TCG	ACG	ACG	ATT	GGG	CCC	528
Asp	Phe	Arg	Gly	His	Gly	Glu	Ser	Gly	Gly	Ser	Thr	Thr	Ile	Gly	Pro	
165										170				175		
CGG	GAG	GTG	CTG	GAT	GCC	CGG	GCT	GTG	GTG	GGC	TAT	GTC	TCG	GAG	CGG	576
Arg	Glu	Val	Leu	Asp	Ala	Arg	Ala	Val	Val	Gly	Tyr	Val	Ser	Glu	Arg	
180								185				190				
TTC	CCC	GGC	CGC	CGG	ATA	ATA	TTG	GTG	GGG	TTC	AGT	ATG	GGC	GGC	GCT	624
Phe	Pro	Gly	Arg	Arg	Ile	Ile	Leu	Val	Gly	Phe	Ser	Met	Gly	Gly	Ala	
195							200				205					
GTA	GCG	ATC	GTG	GAG	GGT	GCT	GGG	GAC	CCG	CGG	GTC	TAC	GCG	GTG	GCT	672
Val	Ala	Ile	Val	Glu	Gly	Ala	Gly	Asp	Pro	Arg	Val	Tyr	Ala	Val	Ala	
210						215				220						
GCT	GAT	AGC	CCG	TAC	TAT	AGG	CTC	CGG	GAC	GTC	ATA	CCC	CGG	TGG	CTG	720
Ala	Asp	Ser	Pro	Tyr	Tyr	Arg	Leu	Arg	Asp	Val	Ile	Pro	Arg	Trp	Leu	
225						230			235					240		
GAG	TAC	AAG	ACG	CCG	CTG	CCG	GGC	TGG	GTG	GGT	GTG	CTG	GCC	GGG	TTC	768
Glu	Tyr	Lys	Thr	Pro	Leu	Pro	Gly	Trp	Val	Gly	Val	Leu	Ala	Gly	Phe	
245							250				255					
TAC	GGG	AGG	CTG	ATG	GCG	GGC	GTT	GAC	CTC	GGC	TTC	GGC	CCC	GCT	GGG	816
Tyr	Gly	Arg	Leu	Met	Ala	Gly	Val	Asp	Leu	Gly	Phe	Gly	Pro	Ala	Gly	
260							265				270					
GTG	GAG	CGC	GTG	GAT	AAG	CCG	TTG	CTG	GTG	GTG	TAT	GGG	CCC	CGG	GAC	864
Val	Gly	Arg	Val	Asp	Lys	Pro	Leu	Leu	Val	Val	Tyr	Gly	Pro	Arg	Asp	
275							280				285					
CCG	CTG	GTG	ACG	CGG	GAC	GAG	GCG	AGG	AGC	CTG	GCG	TCC	CGT	AGC	CCG	912
Pro	Leu	Val	Thr	Arg	Asp	Glu	Ala	Arg	Ser	Leu	Ala	Ser	Arg	Ser	Pro	
290						295			300							
TGT	GGC	CGT	CTC	GTC	GAG	GTT	CCT	GGG	GCT	GGC	CAC	GTG	GAG	GCC	GTG	960
Cys	Gly	Arg	Leu	Val	Glu	Val	Pro	Gly	Ala	Gly	His	Val	Glu	Ala	Val	
305						310			315					320		
GAT	GTG	CTC	GGG	CCG	GGC	CGC	TAC	GCA	GAC	ATG	CTG	ATA	GAG	CTG	GCG	1008
Asp	Val	Leu	Gly	Pro	Gly	Arg	Tyr	Ala	Asp	Met	Leu	Ile	Glu	Leu	Ala	
325							330				335					
CAC	GAG	GAG	TGC	CCT	CCG	GGG	GCC	GGT	GGC	TGA						1019
His	Glu	Glu	Cys	Pro	Pro	Gly	Ala	Gly	Gly							
340							345									

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 789 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATG CCA TAT GTT AGG AAT GGT GGT GTA AAT ATC TAT TAT GAA CTG GTG Met Pro Tyr Val Arg Asn Gly Gly Val Asn Ile Tyr Tyr Glu Leu Val 1 5 10 15	48
GAT GGA CCT GAG CCA CCA ATT GTC TTT GTT CAC GGA TGG ACA GCA AAT Asp Gly Pro Glu Pro Pro Ile Val Phe Val His Gly Trp Thr Ala Asn 20 25 30	96
ATG AAT TTT TGG AAA GAG CAA AGA CGT TAT TTT GCA GGC AGG AAT ATG Met Asn Phe Trp Lys Glu Gln Arg Arg Tyr Phe Ala Gly Arg Asn Met 35 40 45	144
ATG TTG TTT GTC GAT AAC AGA GGT CAT GGC AGG TCC GAT AAG CCA CTT Met Leu Phe Val Asp Asn Arg Gly His Gly Arg Ser Asp Lys Pro Leu 50 55 60	192
GGA TAC GAT TTC TAC AGA TTT GAG AAC TTC ATT TCA GAT TTA GAT GCG Gly Tyr Asp Phe Tyr Arg Phe Glu Asn Phe Ile Ser Asp Leu Asp Ala 65 70 75 80	240
GTT GTT AGG GAG ACT GGA GTG GAG AAA TTT GTT CTC GTC GGA CAT TCA Val Val Arg Glu Thr Gly Val Glu Lys Phe Cal Leu Val Gly His Ser 85 90 95	288
TTC GGA ACA ATG ATC TCT ATG AAG TAC TGT TCG GAG TAT CCG AAT CGG Phe Gly Thr Met Ile Ser Met Lys Tyr Cys Ser Glu Tyr Arg Asn Arg 100 105 110	336
GTT CTT GCT CTA ATC CTC ATA GGT GGT GGG AGC AGA ATA AAG CTT CTA Val Leu Ala Leu Ile Leu Ile Gly Gly Ser Arg Ile Lys Leu Leu 115 120 125	384
CAC AGA ATT GGA TAT CCT TTA GCA AAG ATT CTT GCA TCC ATT GCA TAC His Arg Ile Gly Tyr Pro Leu Ala Lys Ile Leu Ala Ser Ile Ala Tyr 130 135 140	432
AAG AAG TCT TCA AGA TTG GTC GCA GAT CTT TCC TTT GGC AAA AAT GCT Lys Lys Ser Ser Arg Leu Val Ala Asp Leu Ser Phe Gly Lys Asn Ala 145 150 155 160	480
GGT GAA CTT AAA GAG TGG GGA TGG AAA CAG GCA ATG GAT TAT ACA CCC Gly Glu Leu Lys Glu Trp Gly Trp Lys Gln Ala Met Asp Tyr Thr Pro 165 170 175	528
TCC TAC GTG GCA ATG GAC ACG TAC AGA ACT CTA ACG AAA GTG AAT CTT Ser Tyr Val Ala Met Tyr Thr Tyr Arg Thr Leu Thr Lys Val Asn Leu 180 185 190	576
GAA AAT ATC TTG GAG AAA ATA GAC TGT CCA ACA CTG ATT ATC GTT GGA Glu Asn Ile Leu Glu Lys Ile Asp Cys Pro Thr Leu Ile Ile Val Gly 195 200 205	624
GAA GAG GAT GCA CTA TTG CCC GTT AGC AAA TCA GTT GAG CTG AGC AGG Glu Glu Asp Ala Leu Leu Pro Val Ser Lys Ser Val Glu Leu Ser Arg 210 215 220	672
AGG ATA GAA AAC TCA AAG CTT GTG ATC ATC CCA AAC TCG GGG CAT TGC Arg Ile Glu Asn Ser Lys Leu Val Ile Ile Pro Asn Ser Gly His Cys 225 230 235 240	720
GTA ATG CTT GAG AGT CCA AGT GAG GTT AAT AGA GCA ATG GAC GAA TTC Val Met Leu Glu Ser Pro Ser Glu Val Asn Arg Ala Met Asp Glu Phe 245 250 255	768

ATT TCT TCA GCA CAG TTC TAA
 Ile Ser Ser Ala Gln Phe
 260

774

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 756 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTG AGA TTG AGG AAA TTT GAA GAG ATA AAC CTC GTT CTT TCG GGA GGA
 Leu Arg Leu Arg Lys Phe Glu Glu Ile Asn Leu Val Leu Ser Gly Gly
 1 5 10 15

48

GCT GCA AAG GGC ATA GCC CAC ATA GGT GTT TTG AAA GCT ATA AAC GAG
 Ala Ala Lys Gly Ile Ala His Ile Gly Val Leu Lys Ala Ile Asn Glu
 20 25 30

96

CTC GGT ATA AGG GTG AGG GCT TTA AGC GGG GTG AGC GCC GGG GCA ATC
 Leu Glu Ile Arg Val Arg Ala Leu Ser Gly Val Ser Ala Gly Ala Ile
 35 40 45

144

GTT TCG GTC TTT TAT GCC TCA GGC TAC TCC CCT GAA GGG ATG TTC AGC
 Val Ser Val Phe Tyr Ala Ser Gly Tyr Ser Pro Glu Gly Met Phe Ser
 50 55 60

192

CTT CTG AAG AGG GTA AAC TGG CTG AAG CTG TTT AAG TTC AAG CCA CCT
 Leu Leu Lys Arg Val Asn Trp Leu Lys Leu Phe Lys Phe Lye Pro Pro
 65 70 75 80

240

CTG AAG GGA TTG ATA GGG TGG GAG AAG GCT ATA AGA TTC CTT GAG GAA
 Leu Lys Gly Leu Ile Gly Trp Glu Lys Ala Ile Arg Phe Leu Glu Glu
 85 90 95

288

GTT CTC CCT TAC AGG AGA ATA GAA AAA CTT GAG ATA CCG ACG TAT ATA
 Val Leu Pro Tyr Arg Arg Ile Glu Lys Leu GLu Ile Pro Thr Tyr Ile
 100 105 110

336

TGC GCG ACG GAT TTA TAC TCG GGA AGG GCT CTA TAC CTC TCG GAA GGG
 Cys Ala Thr Asp Leu Tyr Ser Gly Arg Ala Leu Tyr Leu SER Glu Gly
 115 120 125

384

AGT TTA ATC CCC GCA CTT CTC GGC AGC TGT GCA ATT CCC GGC ATA TTT
 Ser Leu Ile Pro Ala Leu Leu Gly Ser Cys Ala Ile Pro Gly Ile Phe
 130 135 140

432

GAA CCC GTT GAG TAT AAG AAT TAC TTG CTC GTT GAC GGA GGT ATA GTT
 Glu Pro Val Glu Tyr Lys Asn Tyr Leu Leu Val Asp Gly Gly Ile Val
 145 150 155 160

480

AAC AAC CTT CCC GTT GAG CCC TTT CAG GAA AGC GGT ATT CCC ACC GTT
 Asn Asn Leu Pro Val Glu Pro Phe Gln Glu Ser Gly Ile Pro Thr Val
 165 170 175

528

TGC GTT GAT GTC CTT CCC ATA GAG CCG GAA AAG GAT ATA AAG AAC ATT
 Cys Val Asp Val Leu Pro Ile Glu Pro Glu Lys Asp Ile Lys Asn Ile
 180 185 190

576

CTT CAC ATC CTT TTG AGG AGC TTC TTT CTT GCG GTC CGC TCA AAC TCC Leu His Ile Leu Leu Arg Ser Phe Phe Leu Ala Val Arg Ser Asn Ser 195 200 205	624
GAA AAG AGA AAG GAG TTT TGT GAC CTC GTT ATA GTT CCT GAG CTT GAG Glu Lys Arg Lys Glu Phe Cys Asp Leu Val Ile Val Pro Glu Leu Glu 210 215 220	672
GAG TTC ACA CCC CTT GAT GTT AGA AAA GCG GAC CAA ATA ATG GAG AGG Glu Phe Thr Pro Leu Asp Val Arg Lys Ala Asp Gln Ile Met Glu Arg 225 230 235 240	720
GGA TAC ATA AAG GCC TTA GAG TGA CTT TCT GAA TAG Gly Tyr Ile Lys Ala Leu Glu Val Leu Ser Glu 245 250	768

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 894 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATG TTT AAT ATC AAT GTC TTT GTT AAT ATA TCT TGG CTG TAT TTT TCA Met Phe Asn Ile Asn Val Phe Val Asn Ile Ser Trp Leu Tyr Phe Ser 1 5 10 15	48
GGG ATA GTT ATG AAG ACT GTG GAA GAG TAT GCG CTA CTT GAA ACA GGC Gly Ile Val Met Lys Thr Val Glu Glu Tyr Ala Leu Leu Glu Thr Gly 20 25 30	96
GTA AGA GTG TTT TAT CGG TGT GTA ATC CCG GAG AAA GCT TTT AAC ACT Val Arg Val Phe Tyr Arg Cys Val Ile Pro Glu Lys Ala Phe Asn Thr 35 40 45	144
TTG ATA ATA GGT TCA CAC GGA TTG GGG GCG CAC AGT GGA ATC TAC ATT Leu Ile Ile Gly Ser His Gly Leu Gly Ala His Ser Gly Ile Tyr Ile 50 55 60	192
AGT GTT GCT GAA GAA TTT GCT AGG CAC GGA TTT GGA TTC TGC ATG CAC Ser Val Ala Glu Glu Phe Ala Arg His Gly Phe Gly Phe Cys Met His 65 70 75 80	240
GAT CAA AGG GGA CAT GGG AGA ACG GCA AGC GAT AGA GAA AGA GGG TAT Asp Gln Arg Gly His Gly Arg Thr Ala Ser Asp Arg Glu Arg Gly Tyr 85 90 95	288
GTG GAG GGC TTT CAC AAC TTC ATA GAG GAT ATG AAG GCC TTC TCC GAT Val Glu Gly Phe His Asn Phe Ile Glu Asp Met Lys Ala Phe Ser Asp 100 105 110	336
TAT GCC AAG TGG CGC GTG GGA GGT GAC GAA ATA ATA TTG CTA GGA CAC Tyr Ala Lys Trp Arg Val Gly Asp Glu Ile Ile Leu Leu Gly His 115 120 125	384
AGT ATG GGC GGG CTG ATA GCG CTC GGA ACA GTT GCA ACT TAT AAA GAA Ser Met Gly Gly Leu Ile Ala Leu Leu Thr Val Ala Thr Tyr Lys Glu	432

130	135	140														
ATC	GCC	AAG	GGA	GTT	ATC	GCG	CTA	GCC	CCG	GCC	CTC	CAA	ATC	CCC	TTA	480
Ile	Ala	Lys	Gly	Val	Ile	Ala	Leu	Ala	Pro	Ala	Leu	Gln	Ile	Pro	Leu	
145				150				155					160			
ACC	CCG	GCT	AGA	AGA	CTT	GTT	CTA	AGC	CTC	GCG	TCA	AGG	CTT	GCC	CCG	528
Thr	Pro	Ala	Arg	Arg												
					165				170				175			
CAT	TCT	AAG	ATC	ACC	TTA	CAA	AGG	AGA	TTG	CCG	CAG	AAA	CCA	GAG	GGT	576
His	Ser	Lys	Ile	Thr	Leu	Gln	Arg	Arg	Leu	Pro	Gln	Lys	Pro	Glu	Gly	
					180			185				190				
TTT	CAA	AGA	GCA	AAA	GAT	ATA	GAA	TAC	AGT	CTG	AGT	GAA	ATA	TCA	GTC	624
Phe	Gln	Arg	Ala	Lys	Asp	Ile	Glu	Tyr	Ser	Leu	Ser	Glu	Ile	Ser	Val	
					195			200			205					
AAG	CTC	GTG	GAC	GAA	ATG	ATT	AAA	GCA	TCA	TCT	ATG	TCT	TGG	ACC	ATA	672
Lys	Leu	Val	Asp	Glu	Met	Ile	Lys	Ala	Ser	Ser	Met	Phe	Trp	Thr	Ile	
					210			215			220					
GCA	GGG	GAA	ATT	AAT	ACT	CCC	GTC	CTG	CTT	ATT	CAT	GGG	GAA	AAA	CAG	720
Ala	Gly	Glu	Ile	Asn	Thr	Pro	Val	Leu	Leu	Ile	His	Gly	Glu	Lys	Asp	
					225			230			235			240		
AAT	GTC	ATA	CCT	CCG	GAG	GCG	AGC	AAA	AAA	GCC	RTAC	CAA	TTA	ATA	CCT	768
Asn	Val	Ile	Pro	Pro	Glu	Ala	Ser	Lys	Lys	Als	Tyr	Gln	Leu	Ile	Pro	
					245			250			255					
TCA	TTC	CCT	AAA	GAG	TTG	AAA	AAA	TAC	CCC	GAT	CTT	GGA	CAC	AAC	TTG	816
Ser	Phe	Pro	Lys	Glu	Leu	Lys	Ile	Tyr	Pro	Asp	Leu	Gly	His	Asn	Leu	
					260			265			270					
TTT	TTT	GAA	CCA	GGC	GCG	GTG	AAA	ATC	GTC	ACA	GAC	ATT	GTA	GAG	TGG	864
Phe	Phe	Glu	Pro	Gly	Ala	Val	Lys	Ile	Val	Thr	Asp	Ile	Val	Glu	Trp	
					275			280			285					
GT	T	AAG	AAT	CTA	CCC	AGG	GAA	AAT	CCT	TAA						874
Val	Lys	Asn	Leu	Pro	Arg	Glu	Asn	Pro								
					290			295								

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 789 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATG GAG GTT TAC AAG GCC AAA TTC GGC GAA GCA AAG CTC GGC TGG GTC
Met Glu Val Tyr Lys Ala Lys Phe Gly Ala Lys Leu Gly Trp Val
1 5 10 15

48

GTT CTG GTT CAT GGC CTC GGC GAG CAC AGC GGA AGG TAT GGA AGA CTG
Val Leu Val His Gly Leu Gly Glu His Ser Gly Arg Tyr Gly Arg Leu
20 25 30

96

ATT AAG GAA CTC AAC TAT GCC GGC TTT GGA GTT TAC ACC TTC GAC TGG
Ile Lys Glu Leu Asn Tyr Ala Gly Phe Gly Val Tyr Thr Phe Asp Trp

144

35

40

45

CCC GGC CAC GGG AAG AGC CCG GGC AAG AGA GGG CAC ACG AGC GTC GAG Pro Gly His Gly Lys Ser Pro Gly Lys Arg Gly His Thr Ser Val Glu 50 55 60	192
GAG GCG ATG GAA ATC ATC GAC TCG ATA ATC GAG GAG ATC AGG GAG AAG Glu Ala Met Glu Ile Ile Asp Ser Ile Ile Glu Glu Ile Arg Glu Lys 65 70 75 80	240
CCC TTC CTC TTC GGC CAC AGC CTC GGT GGT CTA ACT GTC ATC AGG TAC Pro Phe Leu Phe Gly His Ser Leu Gly Gly Leu Thr Val Ile Arg Tyr 85 90 95	288
GCT GAG ACG CGG CCC GAT AAA ATA CGG GGA TTA ATA GCT TCC TCG CCT Ala Glu Thr Arg Pro Asp Lys Ile Arg Gly Leu Ile Ala Ser Ser Pro 100 105 110	336
GCC CTC GCC AAG AGC CCG GAA ACG CCG GGC TTC ATG GTG GCC CTC GCG Ala Leu Ala Lys Ser Pro Glu Thr Pro Gly Phe Met Val Ala Leu Ala 115 120 125	384
AAG TTC CTT GGA AAG ATC GCC CCG GGA GTT GTT CTC TCC AAC GGC ATA Lys Phe Leu Gly Lys Ile Ala Pro Gly Val Val Leu Ser Asn Gly Ile 130 135 140	432
AAG CCG GAA CTC CTC TCG AGG AAC AGG GAC GCC GTG AGG AGG TAC GTT Lys Pro Glu Leu Leu Ser Arg Asn Arg Asp Ala Val Arg Arg Tyr Val 145 150 155 160	480
GAA GAC CCA CTC GRC CAC GAC AGG ATT TCG GCC AAG CTG GGA AGG AGC Glu Asp Pro Leu Val His Asp Arg Ile Ser Ala Lys Leu Gly Arg Ser 165 170 175	528
ATC TTC GTG AAC ATG GAG CTG GCC CAC AGG GAG GCG GAC AAG ATA AAA Ile Phe Val Asn Met Glu Leu Ala His Arg Glu Ala Asp Lys Ile Lys 180 185 190	576
GTC CCG ATC CTC CTT CTG ATC GGC ACT GGC GAT GTA ATA ACC CCG CCT Val Pro Ile Leu Leu Ile Gly Thr Gly Asp Val Ile Thr Pro Pro 195 200 205	624
GAA GGC TCA CGC AGA CTC TTC GAG GAG CTG GCC GTC GAG AAC AAA ACC Glu Gly Ser ARg Arg Leu Phe Glu Glu Leu Ala Val Glu Asn Lys Thr 210 215 220	672
CTG AGG GAG TTC GAG GGG GCG TAC CAC GAG ATA TTT GAA GAC CCC GAG Leu Arg Glu Phe Glu Gly Ala Tyr His Glu Ile Phe Glu Asp Pro Glu 225 230 235 240	720
TGG GCC GAG GAG TTC CAC GAA ACA ATT GTT AAG TGG CTG GTT GAA AAA Trp Ala Glu Glu Phe His Glu Thr Ile Val Lys Trp Leu Val Glu Lys 245 250 255	768
TCG TAC TCT TCG GCT CAA TAA Ser Tyr Ser Ser Ala Gln 260	775

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 750 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTG ATT GGC AAT TTG AAA TTG AAG AGG TTT GAA GAG GTT AAC TTA GTT	48
Leu Ile Gly Asn Leu Lys Ley Lys Arg Phe Glu Glu Val Asn Leu Val	
1 5 10 15	
CTT TCG GGA GGG GCT GCC AAG GGT ATC GCC CAT ATA GGT GTT TTA AAA	96
Leu Ser Gly Gly Ala Ala Lys Gly Ile Ala His Ile Gly Val Leu Lys	
20 25 30	
GCT CTG GAA GAG CTC GGT ATA AAG GTA AAG AGG CTC AGC GGG GTA AGT	144
Ala Leu Glu Glu Leu Gly Ile Lys Val Lys Arg Leu Ser Gly Val Ser	
35 40 45	
GCT GGA GCT ATC GTT TCC GTC TTT TAC GCT TCG GGC TAC ACT CCC GAC	192
Ala Gly Ala Ile Val Ser Val Phe Tyr Ala Ser Gly Tyr Thr Pro Asp	
50 55 60	
GAG ATG TTA AAA CTC CTG AAA GAG GTA AAC TGG CTC AAA CTT TTT AAG	240
Glu Met Leu Lys Leu Leu Lys Glu Val Asn Trp Leu Lys Leu Phe Lys	
65 70 75 80	
TTC AAA ACA CCG AAA ATG GGC TTA ATG GGG TGG GAG AAG GCT GCA GAG	288
Phe Lys Thr Pro Lys Met Gly Leu Met Gly Trp Glu Lys Ala Ala Glu	
85 90 95	
TTT TTG TAA AAA GAG CTC GGA GTT AAG AGG CTG GAA GAC CTG AAC ATA	336
Phe Leu Glu Lys Glu Leu Gly Val Lys Arg Leu Glu Asp Leu Asn Ile	
100 105 110	
CCA ACC TAT CTT TGC TCG GCG GAT CTG TAC ACG GGA AAG GCT CTT TAC	384
Pro Thr Tyr Leu Cys Ser Ala Asp Ley Tyr Thr Gly Lys Ala Leu Tyr	
115 120 125	
TTC GGC AGA GGT GAC TTA ATT CCC GTG CTT CTC GGA AGT TGT TCC ATA	432
Phe Gly Arg Gly Asp Leu Ile Pro Val Leu Leu Gly Ser Lys Ser Ile	
130 135 140	
CCC GGG ATT TTT GAA CCA GTT GAG TAC GAG AAT TTT CTA CTT GTT GAC	480
Pro Gly Ile Phe Glu Pro Val Glu Tyr Glu Asn Phe Leu Leu Val Asp	
145 150 155 160	
GGA GGT ATA GTG AAC AAC CTG CCC GTA GAA CCT TTG GAA AAG TTC AAA	528
Gly Gly Ile Val Asn Asn Leu Pro Val Glu Pro Leu Glu Lys Phe Lys	
165 170 175	
GAA CCC ATA ATC GGG GTA GAT GTG CTT CCC ATA ACT CAA GAA AGA AAG	576
Glu Pro Ile Ile Gly Val Asp Val Leu Pro Ile Thr Gln Glu Arg Lys	
180 185 190	
ATT AAA AAT ATA CTC CAC ATC CTT ATA AGG AGC TTC TTT CTG GCG GTT	624
Ile Lye Asn Ile Leu His Ile Leu Ile Arg Ser Phe Phe Leu Ala Val	
195 200 205	
CGT TCC AAT TCG GAA AAG AGA AAG GAG TTC TGC AAC GTA GTT ATA GAA	672
Arg SER Asn Ser Glu Lys Arg Lys Glu Phe Cys Asn Val Val Ile Glu	
210 215 220	
CCT CCC CTT GAA GAG TTC TCT CCT CTG GAC GTA AAT AAG GCG GAC GAG	720
Pro Pro Leu Glu Phe Ser Pro Leu Asp Val Asn Lys Ala Asp Glu	

225

230

235

240

ATA TTC TGC GGG GAT ATG AGA GCA CTT TAA
 Ile Phe Cys Gly Asp Met Arg Ala Leu
 245

730

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 1017 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATG CCA GCT AAT GAC TCA CCC ACG ATC GAC TTT AAT CCT CGC GGC ATT
 Met Pro Ala Asn Asp Ser Pro Thr Ile Asp Phe Asn Pro Arg Gly Ile
 1 5 10 15

48

CTT CGC AAC GCT CAC GCA CAG GTT ATT TTA GCG ACT TCC GGC TTG CGC
 Leu Arg Asn Ala His Ala Gln Val Ile Leu Ala Thr Ser Gly Leu Arg
 20 25 30

96

AAA GCG TTT TTG AAA CGC ACG CAC AAG AGC TAC CTC AGC ACT GCC CAA
 Lys Ala Phe Leu Lys Arg Thr His Lys Ser Tyr Leu Ser Thr Ala Gln
 35 40 45

144

TGG CTG GAG CTC GAT GCC GGC AAC GGA GTT ACC TTG GCC GGA GAG CTT
 Trp Leu Glu Leu Asp Ala Gly Asn Gly Val Thr Leu Ala Gly Glu Leu
 50 55 60

192

AAC ACA GCG CCT GCA ACT GCA TCC TCC CAC CCG GCG CAC AAG AAC 240
 Asn Thr Ala Pro Ala Thr Ala Ser Ser His Pro Ala His Lys Asn
 65 70 75 80

ACT CTG GTT ATT GTG CTG CAC GGC TGG GAA GGC TCC AGC CAG TCG GCC
 Thr Leu Val Ile Val Leu His Gly Trp Glu Gly Ser Ser Gln Ser Ala
 85 90 95

288

TAT GCG ACC TCC GCT GGC AGC ACG CTT TTC GAC AAT GGG TTC GAC ACT
 Tyr Ala Thr Ser Ala Gly Ser Thr Leu Phe Asp Asn Gly Phe Asp Thr
 100 105 110

336

TTT CGC CTT AAT TTT CGC GAT CAC GGC GAC ACC TAC CAC TTA AAC CGC
 Phe Arg Leu Asn Phe Arg Asp His Gly Asp Thr Tyr His Leu Asn Arg
 115 120 125

384

GGC ATA TTT AAC TCA TCG CTG ATT GAC GAA GTA GTG GGC GCA GTC AAA
 Gly Ile Phe Asn Ser Ser Leu Ile Asp Glu Val Val Gly Ala Val Lys
 130 135 140

432

GCC ATC CAG CAG CAA ACC GAC TAC GAC AAG TAT TGC CTG ATG GGG TTC
 Ala Ile Gln Gln Gln Thr Asp Tyr Asp Lys Tyr Cys Leu Met Gly Phe
 145 150 155 160

480

TCA CTG GGT GGG AAC TTT GCC TTG CGC GTC GCG GTG CGG GAA CAG CAT
 Ser Leu Gly Gly Asn Phe Ala Leu Arg Val Ala Val Arg Glu Gln His
 165 170 175

528

CTC GCT AAA CCG CTA GCG GGC GTG CTC GCC GTA TGC CCG GTA CTC GAC Leu Ala Lys Pro Leu Ala Gly Val Leu Ala Val Cys Pro Val Leu Asp 180 185 190	576
CCC GCA CAC ACC ATG ATG GCC CTA AAC CGA GGT GCG TTT TTC TAC GGC Pro Ala His Thr Met Met Ala Leu Asn Arg Gly Ala Phe Phe Tyr Gly 195 200 205	624
CGC TAT TTT GCG CAT AAA TGG AAG CGC TCG TTA ACC GCA AAA CTT GCA Arg Tyr Phe Ala His Lys Trp Lys Arg Ser Leu Thr Ala Lys Leu Ala 210 215 220 225	672
GCT TTC CCA GAC TAC AAA TAC GGC AAA GAT TTA AAA TCG ATA CAC ACG Ala Phe Pro Asp Tyr Lys Tyr Gly Lys Asp Leu Lys Ser Ile His Thr 230 235 240	720
CTT GAT GAG TTA AAC AAC TAT TTC ATT CCC CGC TAC ACC GGC TTC AAC Leu Asp Glu Leu Asn Asn Tyr Phe Ile Pro Arg Tyr Thr Gly Phe Asn 245 250 255	768
TCA GTC TCC GAA TAC TTC AAA AGT TAC ACG CTC ACC GGG CAG AAG CTC Ser Val Ser Glu Tyr Phe Lys Ser Tyr Thr Leu Thr Gly Gln Lys Leu 260 265 270	816
GCG TTT CTC AAC TGC CCC AGT TAC ATT CTG GCA GCT GGC GAC GAC CCA Ala Phe Leu Asn Cys Pro Ser Tyr Ile Leu Ala Ala Gly Asp Asp Pro 275 280 285	864
ATA ATT CCA GCA TCC GAC TTT CAG AAA ATA GCC AAG CCT GCG AAT CTG Ile Ile Pro Ala Ser Asp Phe Gln Lys Ile Ala Lys Pro Ala Asn Leu 290 295 300 305	912
CAC ATA ACA GTA ACG CAA CAA GGT TCT CAT TGC GCA TAC CTG GAA AAC His Ile Thr Val Thr Gln Gln Gly Ser His Cys Ala Tyr Leu Glu Asn 310 315 320	960
CTG CAT AAA CCT AGT GCT GCC GAC AAA TAT GCG GTG AAA TTA TTT GGA Leu His Lys Pro Ser Ala Ala Asp Lys Tyr Ala Val Lys Leu Phe Gly 325 330 335	1,008
GCC TGT TGA Ala Cys	1,111

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 936 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: GENOMIC DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATG CTT GAT ATG CCA ATC GAC CCT GTT TAC TAC CAG CTT GCT GAG TAT Met Leu Asp Met Pro Ile Asp Pro Val Tyr Tyr Gln Leu Ala Glu Tyr 1 5 10 15	48
TTC GAC AGT CTG CCG AAG TTC GAC CAG TTT TCC TCG GCC AGA GAG TAC Phe Asp Ser Leu Pro Lys Phe Asp GLn Phe Ser Ser Ala Arg Glu Tyr 20 25 30	96
AGG GAG GCG ATA AAT CGA ATA TAC GAG GAG AGA AAC CGG CAG CTG AGC	144

Arg Glu Ala Ile Asn Arg Ile Tyr Glu Glu Arg Asn Arg Gln Leu Ser			
35	40	45	
CAG CAT GAG AGG GTT GAA AGA GTT GAG GAC AGG ACG ATT AAG GGG AGG			192
Gln His Glu Arg Val Glu Arg Val Glu Asp Arg Thr Ile Lys Gly Arg			
50	55	60	
AAC GGA GAC ATC AGA GTC AGA GTT TAC CAG CAG AAG CCC GAT TCC CCG			240
Asn Gly Asp Ile Arg Val Arg Val Tyr Gln Gln Lys Pro Asp Ser Pro			
65	70	75	80
GGT CTG GTT TAC TAT CAC GGT GGT GGA TTT GTG ATT TGC AGC ATC GAG			288
Val Leu Val Tyr Tyr His Gly Gly Phe Val Ile Cys Ser Ile Glu			
85	90	95	
TCG CAC GAC GCC TTA TGC AGG AGA AYY GCG AGA CTT TCA AAC TCT ACC			336
Ser HIS Asp Ala Leu Cys Arg ARg Ile Ala Arg Leu Ser Asn Ser Thr			
100	105	110	
GTA GTC TCC GTG GAT TAC AGG CTC GCT CCT GAG CAC AAG TTT CCC CCC			384
Val Val Ser Val Asp Tyr Arg Leu Ala Pro Glu His Lys Phe Pro Ala			
115	120	125	
CCA GTT TAT CAT TGC TAC GAT GCG ACC AAG TGG GTT GCT GAG AAC CGG			432
Ala Val Tyr Asp Cys Tyr Aso Ala Thr Lys Trp Val Ala Glu Asn Ala			
130	135	140	
GAG GAG CTG AGG ATT GAC CCG TCA AAA ATC TTC GTT GGG GGG GAC AGT			480
Glu Glu Leu Arg Ile Asp Pro Ser Lys Ile Phe Val Gly Gly Asp Ser			
145	150	155	160
GCG GGA CGG AAT CTT GCC CCG GCG CTT TCA ATA ATG GCG AGA GAC AGC			528
Ala Gly Gly Asn Leu Ala Ala Ala Val Ser Ile Met Ala Arg Asp Ser			
165	170	175	
GGA GAA GAT TTC ATA AAG CAT CAA ATT CTA ACT TAC CCC GTT GTG AAC			576
Gly Glu Asp Phe Ile Lys His Gln Ile Leu Ile Tyr Pro Val Val Asn			
180	185	190	
TTT GTA GCC CCC ACA CCA TCG CTT CTG GAG TTT GGA GAG GGG CTG TGG			624
Phe Val Ala Pro Thr Pro Ser Leu Leu Glu Phe GLy Glu Gly Leu Trp			
195	200	205	
ATT CTC GAC CAG AAG ATA ATG AGT TGG TTC TCG GAG CAG TAC TTC TCC			672
Ile Leu Asp Gln Lys Ile Met Ser Trp Phe Ser Glu Gln Tyr Phe Ser			
210	215	230	
AGA GAG GAA GAT AAG TTC AAG CCC CTC GCC TCC GTA ATC TTT GCG GAC			720
Arg Glu Glu Aso Lys Phe Asn Pro Leu Ala Ser Val Ile Phe Ala Asp			
235	240	245	250
CTT GAG AAC CTA CCT CCT GCG CTG ATC ATA ACC GCC GAA TAC GAC CCG			768
Leu Glu Asn Leu Pro Pro Ala Leu Ile Ile Thr Ala Glu Tyr Asp Pro			
255	260	265	
CTG AGA GAT GAA GGA GAA GTT TTC GGG CAG ATG CTG AGA AGA GCA GGT			816
Leu Arg Asp Glu Gly Glu Val Phe Gly Gln Met Leu Arg Arg Ala Gly			
270	275	280	
GTT GAG GCG AGC ATC GTC AGA TAC AGA GGC GTG CTT CAC GGA TTC ATC			864
Val Glu Ala Ser Ile Val Arg Tyr Arg Gly Val Leu His Gly Phe Ile			
285	290	295	
AAT TAC TAT CCC GTG CTG AAG GCT GCG AGG GAT GCG ATA AAC CAG ATT			912
Asn Tyr Tyr Pro Val Leu Lys Ala Ala Arg Asp Ala Ile Asn Gln Ile			

300

305

310

GCC GCT CTT CTT GTG TTC GAC TAG
 Ala Ala Leu leu Val Phe Asp
 315 320

936

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 918 NUCLEOTIDES
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: GENOMIC DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATG CCC CTA GAT CCT AGA ATT AAA AAG TTA CTA GAA TCA GCT CTT ACT
 Met Pro Leu Asp Pro Arg Ile Lys Lys Leu Leu Glu Ser Ala Leu Thr
 5 10 15

48

ATA CCA ATT GGT AAA GCC CCA GTA GAA GAG GTA AGA AAG ATA TTT AGG
 Ile Pro Ile Gly Lys Ala Pro Val Glu Glu Val Arg Lys Ile Phe Arg
 20 25 30

96

CAA TTA GCG TCG GCA GCT CCC AAA GTC GAA GTT GGA AAA GTA GAA GAT
 Gln Leu Ala Ser Ala Ala Pro Lys Val Glu Val Gly Lys Val Glu Asp
 35 40 45

144

ATA AAA ATA CCA GGC AGT GAA ACC GTT ATA AAC GCT AGA GTG TAT TTT
 Ile Lys Ile Pro Gly Ser Glu Thr Val Ile Asn Ala Arg Val Tyr Phe
 50 55 60

192

CCG AAG AGT AGC GGT CCT TAT GGT GTT CTA GTG TAT CTT CAT GGA GGC
 Pro Lys Ser Ser Gly Pro Tyr Gly Val Leu Val Tyr Leu His Gly Gly
 65 70 75 80

240

GGT TTT GTA ATA GGC GAT GTG GAA TCT TAT GAC CCA TTA TGT AGA GCA
 Gly Phe Val Ile Gly Asp Val Glu Ser Tyr Asp Pro Leu Cys Arg Ala
 85 90 95

288

ATT ACA AAT GCG TGC AAT TGC GTT GTA GTC TCA GTG GAC TAT AGG TTA
 Ile Thr Asn Ala Cys Asn Cys Val Val Val Ser Val Asp Tyr Arg Leu
 100 105 110

336

GCT CCA GAA TAC AAG TTT CCT TCT GCA GTT ATC GAT TCA TTT GAC GCT
 Ala Pro Glu Tyr Lys Phe Pro Ser Ala Val Ile Asp Ser Phe Asp Ala
 115 120 125

384

ACT AAT TGG GTT TAT AAC AAT TTA GAT AAA TTT GAT GGA AAG ATG GGA
 Thr Asn Trp Val Tyr Asn Asn Leu Asp Lys Phe Asp Gly Lys Met Gly
 130 135 140

432

GTT GCG ATT GCG GGA GAT AGT GCT GGA GGA AAT TTG GCA GCG GTT GTA
 Val Ala Ile Ala Gly Asp Ser Ale Gly Gly Asn Leu Ala Ala Val Val
 145 150 155 160

480

GCT CTT CTT TCA AAG GGT AAA ATT AAT TTG AAG TAT CAA ATA CTG GTT
 Ala Leu Leu Ser Lys Gly Lys Ile Asn Leu Lys Tyr Gln Ile Leu Val
 165 170 175

528

TAC CCA GCG GTA AGT TTA GAT AAC GTT TCA AGA TCC ATG ATA GAG TAC

576

Tyr Pro Ala Val Ser Leu Asp Asn Val Ser Arg Ser Met Ile Glu Tyr			
180	185	190	
TCT GAT GGG TTC TTC CTT ACC AGA GAG CAT ATA GAG TGG TTC GGT TCT		624	
Ser Asp Gly Phe Phe Leu Thr Arg Glu His Ile Glu Trp Phe Gly Ser			
195	200	205	
CAA TAC TTA CGA AGC CCT GCA GAT TTG CTA GAC TTT AGG TTC TCT CCA		672	
Gln Tyr Leu Arg Ser Pro Ala Asp Leu Leu Asp Phe Arg Phe Ser Pro			
210	215	220	
ATT CTG GCG CAA GAT TTC AAC GGA TTA CCT CCA GCC TTG ATA ATA ACA		720	
Ile Leu Ala Gln Asp Phe Asn Gly Leu Pro Pro Ala Leu Ile Ile Thr			
225	230	235	240
GCA GAA TAC GAT CCA CTA AGG GAT CAA GGA GAA GCG TAT GCA AAT AAA		768	
Ala Glu Tyr Asp Pro Leu Arg Asp Gln Gly Glu Ala Tyr Ala Asn Lys			
245	250	255	
CTA CTA CAA GCT GGA GTC TCA GTT ACT AGT GTG AGA TTT AAC AAC GTT		816	
Leu Leu Gln Ala Gly Val Ser Val Thr Ser Val Arg Phe Asn Asn Val			
260	265	270	
ATA CAC GGA TTC CTC TCA TTC TTT CCG TTG ATG GAG CAA GGA AGA GAT		864	
Ile His Gly Phe Leu Ser Phe Phe Pro Leu Met Glu Gln Gly Arg Asp			
275	280	285	
GCT ATA GGT CTG ATA GGG TCT GTG TTA AGA CGA GTA TTT TAT GAT AAA		912	
Ala Ile Gly Leu Ile Gly Ser Val Leu Arg Arg Val Phe Tyr Asp Lys			
290	295	300	
ATT TAA		918	
Ile			
305			

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 184 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Ser Leu Asn Lys His Ser Trp Met Asp Met Ile Ile Phe Ile Leu			
1	5	10	15
Ser Phe Ser Phe Pro Leu Thr Met Ile Ala Leu Ala Ile Ser Met Ser			
20	25	30	
Ser Trp Phe Asn Ile Trp Asn Asn Ala Leu Ser Asp Leu Gly His Ala			
35	40	45	
Val Lys Ser Ser Val Ala Pro Ile Phe Asn Leu Gly Leu Ala Ile Gly			
50	55	60	
Gly Ile Leu Ile Val Ile Val Gly Leu Arg Asn Leu Tyr Ser Trp Ser			
65	70	75	80
Arg Val Lys Gly Ser Leu Ile Ile Ser Met Gly Val Phe Leu Asn Leu			
85	90	95	

Ile Gly Val Phe Asp Glu Val Tyr Gly Trp Ile His Phe Leu Val Ser
 100 105 110
 Val Leu Phe Phe Leu Ser Ile Ile Ala Tyr Phe Ile Ala Ile Ser Ile
 115 120 125
 Leu Asp Lys Ser Trp Ile Ala Val Leu Leu Ile Ile Gly His Ile Ala
 130 135 140
 Met Trp Tyr Leu His Phe Ala Ser Glu Ile Pro Arg Gly Ala Ala Ile
 145 150 155 160
 Pro Glu Leu Leu Ala Val Phe Ser Phe Leu Pro Phe Tyr Ile Arg Asp
 165 170 175
 Tyr Phe Lys Ser Tyr Thr Lys Arg
 180

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 346 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Lys Leu Leu Glu Pro Thr Asn Thr Ser Tyr Thr Leu Leu Gln Asp
 1 5 10 15
 Leu Ala Leu His Phe Ala Phe Tyr Trp Phe Leu Ala Val TYr Thr Trp
 20 25 30
 Leu Pro Gly Val Leu Val Arg Gly Val Ala Val Asp Thr Gly Val Ala
 35 40 45
 Arg Val Pro Gly Leu Gly Arg Arg Gly Lys Arg Leu Leu Leu Ala Ala
 50 55 60
 Val Ala Val Leu Ala Leu Val Val Ser Val Val Val Pro Ala Tyr Val
 65 70 75 80
 Ala Tyr Ser Ser Leu His Pro Glu Ser Cys Arg Pro Val Ala Pro Glu
 85 90 95
 Gly Leu Thr Tyr Lys Glu Phe Ser Val Thr Ala Glu Asp Gly Leu Val
 100 105 110
 Val Arg Gly Trp Cal Leu Gly Pro Gly Ala Gly Gly Asn Pro Val Phe
 115 120 125
 Val Leu Met His Gly Tyr Thr Gly Cys Arg Ser Ala Pro Tyr Met Ala
 130 135 140
 Val Leu Ala Arg Glu Leu Val Glu Trp Gly Tyr Pro Val Val Val Phe
 145 150 155 160
 Asp Phe Arg Gly His Gly Glu Ser Gly Gly Ser Thr Thr Ile Gly Pro
 165 170 175
 Arg Glu Val Leu Asp Ala Arg Ala Val Val Gly Tyr Val Ser Glu Arg
 180 185 190

Phe Pro Gly Arg Arg Ile Ile Leu Val Gly Phe Ser Met Gly Gly Ala
 195 200 205
 Val Ala Ile Val Glu Gly Ala Gly Asp Pro Arg Val Tyr Ala Val Ala
 210 215 220
 Ala Asp Ser Pro Tyr Tyr Arg Leu Arg Asp Val Ile Pro Arg Trp Leu
 225 230 235 240
 Glu Tyr Lys Thr Pro Leu Pro Gly Trp Val Gly Val Leu Ala Gly Phe
 245 250 255
 Tyr Gly Arg Leu Met Ala Gly Val Asp Leu Gly Phe Gly Pro Ala Gly
 260 265 270
 Val Gly Arg Val Asp Lys Pro Leu Leu Val Val Tyr Gly Pro Arg Asp
 275 280 285
 Pro Leu Val Thr Arg Asp Glu Ala Arg Ser Leu Ala Ser Arg Ser Pro
 290 295 300
 Cys Gly Arg Leu Val Glu Val Pro Gly Ala Gly His Val Glu Ala Val
 305 310 315 320
 Asp Val Leu Gly Pro Gly Arg Tyr Ala Asp Met Leu Ile Glu Leu Ala
 325 330 335
 His Glu Glu Cys Pro Pro Gly Ala Gly Gly
 340 345

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 262 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: PROTEIN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Pro Tyr Val Arg Asn Gly Gly Val Asn Ile Tyr Tyr Glu Leu Val
 1 5 10 15
 Asp Gly Pro Glu Pro Pro Ile Val Phe Val His Gly Trp Thr Ala Asn
 20 25 30
 Met Asn Phe Trp Lys Glu Gln Arg Arg Tyr Phe Ala Gly Arg Asn Met
 35 40 45
 Met Leu Phe Val Asp Asn Arg Gly His Gly Arg Ser Asp Lys Pro Leu
 50 55 60
 Gly Tyr Asp Phe Tyr Arg Phe Glu Asn Phe Ile Ser Asp Leu Asp Ala
 65 70 75 80
 Val Val Arg Glu Thr Gly Val Glu Lys Phe Val Leu Val Gly His Ser
 85 90 95
 Phe Gly Thr Met Ile Ser Met Lys Tyr Cys Ser Glu Tyr Arg Asn Arg
 100 105 110
 Val Leu Ala Leu Ile Leu Ile Gly Gly Ser Arg Ile Lys Leu Leu

115	120	125
His Arg Ile Gly Tyr Pro Leu Ala Lys Ile Leu Ala Ser Ile Ala Tyr		
130	135	140
Lys Lys Ser Ser Arg Leu Val Ala Asp Leu Ser Phe Gly Lys Asn Ala		
145	150	155
Gly Glu Leu Lys Glu Trp Gly Trp Lys Gln Ala Met Asp Tyr Thr Pro		
165	170	175
Ser Tyr Val Ala Met Tyr Thr Tyr Arg Thr Leu Thr Lys Val Asn Leu		
180	185	190
Glu Asn Ile Leu Glu Lys Ile Asp Cys Pro Thr Leu Ile Ile Val Gly		
195	200	205
Glu Glu Asp Ala Leu Leu Pro Val Ser Lys Ser Val Glu Leu Ser Arg		
210	215	220
Arg Ile Glu Asn Ser Lys Leu Val Ile Ile Pro Asn Ser Gly His Cys		
225	230	235
Val Met Leu Glu Ser Pro Ser Glu Val Asn Arg Ala Met Asp Glu Phe		
245	250	255
Ile Ser Ser Ala Gln Phe		
260		

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 251 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Leu Arg Leu Arg Lys Phe Glu Glu Ile Asn Leu Val Leu Ser Gly Gly		
1	5	10
Ala Ala Lys Gly Ile Ala His Ile Gly Val Leu Lys Ala Ile Asn Glu		
20	25	30
Leu Glu Ile Arg Val Arg Ala Leu Ser Gly Val Ser Ala Gly Ala Ile		
35	40	45
Val Ser Val Phe Tyr Ala Ser Gly Tyr Ser Pro Glu Gly Met Phe Ser		
50	55	60
Leu Leu Lys Arg Val Asn Trp Leu Lys Leu Phe Lys Phe Lye Pro Pro		
65	70	75
Leu Lys Gly Leu Ile Gly Trp Glu Lys Ala Ile Arg Phe Leu Glu Glu		
85	90	95
Val Leu Pro Tyr Arg Arg Ile Glu Lys Leu GLu Ile Pro Thr Tyr Ile		
100	105	110
Cys Ala Thr Asp Leu Tyr Ser Gly Arg Ala Leu Tyr Leu SER Glu Gly		
115	120	125

Ser Leu Ile Pro Ala Leu Leu Gly Ser Cys Ala Ile Pro Gly Ile Phe
 130 135 140
 Glu Pro Val Glu Tyr Lys Asn Tyr Leu Leu Val Asp Gly Gly Ile Val
 145 150 155 160
 Asn Asn Leu Pro Val Glu Pro Phe Gln Glu Ser Gly Ile Pro Thr Val
 165 170 175
 Cys Val Asp Val Leu Pro Ile Glu Pro Glu Lys Asp Ile Lys Asn Ile
 180 185 190
 Leu His Ile Leu Leu Arg Ser Phe Phe Leu Ala Val Arg Ser Asn Ser
 195 200 205
 Glu Lys Arg Lys Glu Phe Cys Asp Leu Val Ile Val Pro Glu Leu Glu
 210 215 220
 Glu Phe Thr Pro Leu Asp Val Arg Lys Ala Asp Gln Ile Met Glu Arg
 225 230 235 240
 Gly Tyr Ile Lys Ala Leu Glu Val Leu Ser Glu
 245 250

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 297 AMINO ACIDS
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Phe Asn Ile Asn Val Phe Val Asn Ile Ser Trp Leu Tyr Phe Ser
 1 5 10 15
 Gly Ile Val Met Lys Thr Val Glu Glu Tyr Ala Leu Leu Glu Thr Gly
 20 25 30
 Val Arg Val Phe Tyr Arg Cys Val Ile Pro Glu Lys Ala Phe Asn Thr
 35 40 45
 Leu Ile Ile Gly Ser His Gly Leu Gly Ala His Ser Gly Ile Tyr Ile
 50 55 60
 Ser Val Ala Glu Glu Phe Ala Arg His Gly Phe Gly Phe Cys Met His
 65 70 75 80
 Asp Gln Arg Gly His Gly Arg Thr Ala Ser Asp Arg Glu Arg Gly Tyr
 85 90 95
 Val Glu Gly Phe His Asn Phe Ile Glu Asp Met Lys Ala Phe Ser Asp
 100 105 110
 Tyr Ala Lys Trp Arg Val Gly Gly Asp Glu Ile Ile Leu Leu Gly His
 115 120 125
 Ser Met Gly Gly Leu Ile Ala Leu Leu Thr Val Ala Thr Tyr Lys Glu
 130 135 140
 Ile Ala Lys Gly Val Ile Ala Leu Ala Pro Ala Leu Gln Ile Pro Leu
 145 150 155 160

Thr Pro Ala Arg Arg Leu Val Leu Ser Leu Ala Ser Arg Leu Ala Pro
 165 170 175
 His Ser Lys Ile Thr Leu Gln Arg Arg Leu Pro Gln Lys Pro Glu Gly
 180 185 190
 Phe Gln Arg Ala Lys Asp Ile Glu Tyr Ser Leu Ser Glu Ile Ser Val
 195 200 205
 Lys Leu Val Asp Glu Met Ile Lys Ala Ser Ser Met Phe Trp Thr Ile
 210 215 220
 Ala Gly Glu Ile Asn Thr Pro Val Leu Leu Ile His Gly Glu Lys Asp
 225 230 235 240
 Asn Val Ile Pro Pro Glu Ala Ser Lys Lys Als Tyr Gln Leu Ile Pro
 245 250 255
 Ser Phe Pro Lys Glu Leu Lys Ile Tyr Pro Asp Leu Gly His Asn Leu
 260 265 270
 Phe Phe Glu Pro Gly Ala Val Lys Ile Val Thr Asp Ile Val Glu Trp
 275 280 285
 Val Lys Asn Leu Pro Arg Glu Asn Pro
 290 295

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 262 AMINO ACIDS
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Glu Val Tyr Lys Ala Lys Phe Gly Glu Ala Lys Leu Gly Trp Val
 1 5 10 15
 Val Leu Val His Gly Leu Gly Glu His Ser Gly Arg Tyr Gly Arg Leu
 20 25 30
 Ile Lys Glu Leu Asn Tyr Ala Gly Phe Gly Val Tyr Thr Phe Asp Trp
 35 40 45
 Pro Gly His Gly Lys Ser Pro Gly Lys Arg Gly His Thr Ser Val Glu
 50 55 60
 Glu Ala Met Glu Ile Ile Asp Ser Ile Ile Glu Glu Ile Arg Glu Lys
 65 70 75 80
 Pro Phe Leu Phe Gly His Ser Leu Gly Gly Leu Thr Val Ile Arg Tyr
 85 90 95
 Ala Glu Thr Arg Pro Asp Lys Ile Arg Gly Leu Ile Ala Ser Ser Pro
 100 105 110
 Ala Leu Ala Lys Ser Pro Glu Thr Pro Gly Phe Met Val Ala Leu Ala
 115 120 125
 Lys Phe Leu Gly Lys Ile Ala Pro Gly Val Val Leu Ser Asn Gly Ile

130	135	140
Lys Pro Glu Leu Leu Ser Arg Asn Arg Asp Ala Val Arg Arg Tyr Val		
145	150	155
Glu Asp Pro Leu Val His Asp Arg Ile Ser Ala Lys Leu Gly Arg Ser		
165	170	175
Ile Phe Val Asn Met Glu Leu Ala His Arg Glu Ala Asp Lys Ile Lys		
180	185	190
Val Pro Ile Leu Leu Ile Gly Thr Gly Asp Val Ile Thr Pro Pro		
195	200	205
Glu Gly Ser ARG Arg Leu Phe Glu Glu Leu Ala Val Glu Asn Lys Thr		
210	215	220
Leu Arg Glu Phe Glu Gly Ala Tyr His Glu Ile Phe Glu Asp Pro Glu		
225	230	235
Trp Ala Glu Glu Phe His Glu Thr Ile Val Lys Trp Leu Val Glu Lys		
245	250	255
Ser Tyr Ser Ser Ala Gln		
260		

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 249 AMINO ACIDS
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Leu Ile Gly Asn Leu Lys Ley Lys Arg Phe Glu Glu Val Asn Leu Val		
1	5	10
Leu Ser Gly Gly Ala Ala Lys Gly Ile Ala His Ile Gly Val Leu Lys		
20	25	30
Ala Leu Glu Glu Leu Gly Ile Lys Val Lys Arg Leu Ser Gly Val Ser		
35	40	45
Ala Gly Ala Ile Val Ser Val Phe Tyr Ala Ser Gly Tyr Thr Pro Asp		
50	55	60
Glu Met Leu Lys Leu Leu Lys Glu Val Asn Trp Leu Lys Leu Phe Lys		
65	70	75
Phe Lys Thr Pro Lys Met Gly Leu Met Gly Trp Glu Lys Ala Ala Glu		
85	90	95
Phe Leu Glu Lys Glu Leu Gly Val Lys Arg Leu Glu Asp Leu Asn Ile		
100	105	110
Pro Thr Tyr Leu Cys Ser Ala Asp Ley Tyr Thr Gly Lys Ala Leu Tyr		
115	120	125
Phe Gly Arg Gly Asp Leu Ile Pro Val Leu Leu Gly Ser Lys Ser Ile		
130	135	140

Pro Gly Ile Phe Glu Pro Val Glu Tyr Glu Asn Phe Leu Leu Val Asp
 145 150 155 160
 Gly Gly Ile Val Asn Asn Leu Pro Val Glu Pro Leu Glu Lys Phe Lys
 165 170 175
 Glu Pro Ile Ile Gly Val Asp Val Leu Pro Ile Thr Gln Glu Arg Lys
 180 185 190
 Ile Lys Asn Ile Leu His Ile Leu Ile Arg Ser Phe Phe Leu Ala Val
 195 200 205
 Arg SER Asn Ser Glu Lys Arg Lys Glu Phe Cys Asn Val Val Ile Glu
 210 215 220
 Pro Pro Leu Glu Glu Phe Ser Pro Leu Asp Val Asn Lys Ala Asp Glu
 225 230 235 240
 Ile Phe Cys Gly Asp Met Arg Ala Leu
 245

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 339 AMINO ACIDS
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Pro Ala Asn Asp Ser Pro Thr Ile Asp Phe Asn Pro Arg Gly Ile
 1 5 10 15
 Leu Arg Asn Ala His Ala Gln Val Ile Leu Ala Thr Ser Gly Leu Arg
 20 25 30
 Lys Ala Phe Leu Lys Arg Thr His Lys Ser Tyr Leu Ser Thr Ala Gln
 35 40 45
 Trp Leu Glu Leu Asp Ala Gly Asn Gly Val Thr Leu Ala Gly Glu Leu
 50 55 60
 Asn Thr Ala Pro Ala Thr Ala Ser Ser Ser His Pro Ala His Lys Asn
 65 70 75 80
 Thr Leu Val Ile Val Leu His Gly Trp Glu Gly Ser Ser Gln Ser Ala
 85 90 95
 Tyr Ala Thr Ser Ala Gly Ser Thr Leu Phe Asp Asn Gly Phe Asp Thr
 100 105 110
 Phe Arg Leu Asn Phe Arg Asp His Gly Asp Thr Tyr His Leu Asn Arg
 115 120 125
 Gly Ile Phe Asn Ser Ser Leu Ile Asp Glu Val Val Gly Ala Val Lys
 130 135 140
 Ala Ile Gln Gln Gln Thr Asp Tyr Asp Lys Tyr Cys Leu Met Gly Phe
 145 150 155 160
 Ser Leu Gly Gly Asn Phe Ala Leu Arg Val Ala Val Arg Glu Gln His
 165 170 175

Leu Ala Lys Pro Leu Ala Gly Val Leu Ala Val Cys Pro Val Leu Asp
 180 185 190
 Pro Ala His Thr Met Met Ala Leu Asn Arg Gly Ala Phe Phe Tyr Gly
 195 200 205
 Arg Tyr Phe Ala His Lys Trp Lys Arg Ser Leu Thr Ala Lys Leu Ala
 210 215 220 225
 Ala Phe Pro Asp Tyr Lys Tyr Gly Lys Asp Leu Lys Ser Ile His Thr
 230 235 240
 Leu Asp Glu Leu Asn Asn Tyr Phe Ile Pro Arg Tyr Thr Gly Phe Asn
 245 250 255
 Ser Val Ser Glu Tyr Phe Lys Ser Tyr Thr Leu Thr Gly Gln Lys Leu
 260 265 270
 Ala Phe Leu Asn Cys Pro Ser Tyr Ile Leu Ala Ala Gly Asp Asp Pro
 275 280 285
 Ile Ile Pro Ala Ser Asp Phe Gln Lys Ile Ala Lys Pro Ala Asn Leu
 290 295 300 305
 His Ile Thr Val Thr Gln Gln Gly Ser His Cys Ala Tyr Leu Glu Asn
 310 315 320
 Leu His Lys Pro Ser Ala Ala Asp Lys Tyr Ala Val Lys Leu Phe Gly
 325 330 335
 Ala Cys

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 311 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met Leu Asp Met Pro Ile Asp Pro Val Tyr Tyr Gln Leu Ala Glu Tyr
 1 5 10 15
 Phe Asp Ser Leu Pro Lys Phe Asp GLn Phe Ser Ser Ala Arg Glu Tyr
 20 25 30
 Arg Glu Ala Ile Asn Arg Ile Tyr Glu Glu Arg Asn Arg Gln Leu Ser
 35 40 45
 Gln His Glu Arg Val Glu Arg Val Glu Asp Arg Thr Ile Lys Gly Arg
 50 55 60
 Asn Gly Asp Ile Arg Val Arg Val Tyr Gln Gln Lys Pro Asp Ser Pro
 65 70 75 80
 Val Leu Val Tyr Tyr His Gly Gly Phe Val Ile Cys Ser Ile Glu
 85 90 95
 Ser HIS Asp Ala Leu Cys Arg ARg Ile Ala Arg Leu Ser Asn Ser Thr
 100 105 110

Val Val Ser Val Asp Tyr Arg Leu Ala Pro Glu His Lys Phe Pro Ala
 115 120 125
 Ala Val Tyr Asp Cys Tyr Asn Ala Thr Lys Trp Val Ala Glu Asn Ala
 130 135 140
 Glu Glu Leu Arg Ile Asp Pro Ser Lys Ile Phe Val Gly Gly Asp Ser
 145 150 155 160
 Ala Gly Gly Asn Leu Ala Ala Val Ser Ile Met Ala Arg Asp Ser
 165 170 175
 Gly Glu Asp Phe Ile Lys His Gln Ile Leu Ile Tyr Pro Val Val Asn
 180 185 190
 Phe Val Ala Pro Thr Pro Ser Leu Leu Glu Phe GLy Glu Gly Leu Trp
 195 200 205
 Ile Leu Asp Gln Lys Ile Met Ser Trp Phe Ser Glu Gln Tyr Phe Ser
 210 215 230
 Arg Glu Glu Asn Lys Phe Asn Pro Leu Ala Ser Val Ile Phe Ala Asp
 235 240 245 250
 Leu Glu Asn Leu Pro Pro Ala Leu Ile Ile Thr Ala Glu Tyr Asp Pro
 255 260 265
 Leu Arg Asp Glu Gly Glu Val Phe Gly Gln Met Leu Arg Arg Ala Gly
 270 275 280
 Val Glu Ala Ser Ile Val Arg Tyr Arg Gly Val Leu His Gly Phe Ile
 285 290 295
 Asn Tyr Tyr Pro Val Leu Lys Ala Ala Arg Asp Ala Ile Asn Gln Ile
 300 305 310
 Ala Ala Leu leu Val Phe Asp
 315 320

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 305 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Pro Leu Asp Pro Arg Ile Lys Lys Leu Leu Glu Ser Ala Leu Thr
 5 10 15
 Ile Pro Ile Gly Lys Ala Pro Val Glu Glu Val Arg Lys Ile Phe Arg
 20 25 30
 Gln Leu Ala Ser Ala Ala Pro Lys Val Glu Val Gly Lys Val Glu Asp
 35 40 45
 Ile Lys Ile Pro Gly Ser Glu Thr Val Ile Asn Ala Arg Val Tyr Phe
 50 55 60

Pro Lys Ser Ser Gly Pro Tyr Gly Val Leu Val Tyr Leu His Gly Gly
65 70 75 80

Gly Phe Val Ile Gly Asp Val Glu Ser Tyr Asp Pro Leu Cys Arg Ala
85 90 95

Ile Thr Asn Ala Cys Asn Cys Val Val Val Ser Val Asp Tyr Arg Leu
100 105 110

Ala Pro Glu Tyr Lys Phe Pro Ser Ala Val Ile Asp Ser Phe Asp Ala
115 120 125

Thr Asn Trp Val Tyr Asn Asn Leu Asp Lys Phe Asp Gly Lys Met Gly
130 135 140

Val Ala Ile Ala Gly Asp Ser Ale Gly Gly Asn Leu Ala Ala Val Val
145 150 155 160

Ala Leu Leu Ser Lys Gly Lys Ile Asn Leu Lys Tyr Gln Ile Leu Val
165 170 175

Tyr Pro Ala Val Ser Leu Asp Asn Val Ser Arg Ser Met Ile Glu Tyr
180 185 190

Ser Asp Gly Phe Phe Leu Thr Arg Glu His Ile Glu Trp Phe Gly Ser
195 200 205

Gln Tyr Leu Arg Ser Pro Ala Asp Leu Leu Asp Phe Arg Phe Ser Pro
210 215 220

Ile Leu Ala Gln Asp Phe Asn Gly Leu Pro Pro Ala Leu Ile Ile Thr
225 230 235 240

Ala Glu Tyr Asp Pro Leu Arg Asp Gln Gly Glu Ala Tyr Ala Asn Lys
245 250 255

Leu Leu Gln Ala Gly Val Ser Val Thr Ser Val Arg Phe Asn Asn Val
260 265 270

Ile His Gly Phe Leu Ser Phe Phe Pro Leu Met Glu Gln Gly Arg Asp
275 280 285

Ala Ile Gly Leu Ile Gly Ser Val Leu Arg Arg Val Phe Tyr Asp Lys
290 295 300

Ile
305